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1647

TECH CENTER 1600/2800

RAW SEQUENCE LISTING

DATE: 02/01/2001

PATENT APPLICATION: US/08/765,588A

TIME: 12:12:02

Input Set : A:\sequence.asc

Output Set: N:\CRF3\02012001\H765588A.raw

ENTERED

#27

4 <110> APPLICANT: Hayward, Nicholas K.
5 Weber, Gunther
6 Grimmond, Sean
7 Nordenskjold, Magnus
8 Larsson, Catharina
10 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
11 SAME
13 <130> FILE REFERENCE: DAVIES
15 <140> CURRENT APPLICATION NUMBER: 08/765,588A
C--> 16 <141> CURRENT FILING DATE: 1997-04-27
18 <160> NUMBER OF SEQ ID NOS: 22
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 649
24 <212> TYPE: DNA
25 <213> ORGANISM: Nucleotide Sequence of YEGF165
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (17)..(589)
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34 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
35 1 5 10
37 gcc ttg ctg ctg tac ctg cac cat gcc aag tgg tcc cag gct gca ccc 100
39 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
40 15 20 25
42 atg gca gaa gga gga gga cag aat cat cac gaa gtg gtg aag ttc atg 148
44 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
45 30 35 40
47 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196
49 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
50 45 50 55 60
52 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244
54 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
55 65 70 75
57 tgt gtg ccc ctg atg cga tgc ggc ggc tgc tgc aat gac gag ggc ctg 292
59 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
60 80 85 90
62 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
64 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
65 95 100 105
67 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cay 388
69 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
70 110 115 120
72 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
74 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
75 125 130 135 140

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77 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
79 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
80      145      150      155
82 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
84 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
85      160      165      170
87 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
89 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
90      175      180      185
92 ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg 629
94 Pro Arg Arg
95      190
97 gaaccagatc tctcaccagg 649
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102 <211> LENGTH: 191
103 <212> TYPE: PRT
104 <213> ORGANISM: Nucleotide Sequence of VEGF165
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110 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
111 20 25 30
113 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
114 35 40 45
116 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
117 50 55 60
119 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
120 65 70 75 80
122 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
123 85 90 95
125 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
126 100 105 110
128 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
129 115 120 125
131 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
132 130 135 140
134 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
135 145 150 155 160
137 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
138 165 170 175
140 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
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147 <212> TYPE: DNA
148 <213> ORGANISM: Nucleotide Sequence of SOM175
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (3)..(623)

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158 1 5 10 15
160 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
162 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
163 20 25 30
165 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
167 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
168 35 40 45
170 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
172 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
173 50 55 60
175 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
177 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
178 65 70 75
180 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
182 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
183 80 85 90 95
185 caa gtc cgg atg cag atc ctc atg atc cgg tac cgc agc agt cag ctg 335
187 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
188 100 105 110
190 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
192 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
193 115 120 125
195 aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
197 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
198 130 135 140
200 cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
202 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
203 145 150 155
205 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
207 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
208 160 165 170 175
210 gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
212 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
213 180 185 190
215 gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
217 Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
218 195 200 205
220 tagagctcaa ccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
223 agactcagca gggtagcttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743
226 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
229 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
232 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
235 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattctaca actggctctt 983
238 cctcccccca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
241 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094
245 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

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TIME: 12:12:02

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Output Set: N:\CRF3\02012001\H765588A.raw

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247 <212> TYPE: PRT
248 <213> ORGANISM: Nucleotide Sequence of SOM175
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254 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
255 20 25 30
257 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
258 35 40 45
260 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
261 50 55 60
263 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
264 65 70 75 80
266 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
267 85 90 95
269 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
270 100 105 110
272 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
273 115 120 125
275 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
276 130 135 140
278 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
279 145 150 155 160
281 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
282 165 170 175
284 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
285 180 185 190
287 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
288 195 200 205
292 <210> SEQ ID NO: 5
293 <211> LENGTH: 993
294 <212> TYPE: DNA
295 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (3)..(566)
301 <400> SEQUENCE: 5
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305 1 5 10 15
307 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
309 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
310 20 25 30
312 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
314 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
315 35 40 45
317 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
319 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr

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322 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
324 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
325          65          70          75
327 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
329 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
330 80          85          90          95
332 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
334 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
335          100          105          110
337 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
339 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
340          115          120          125
342 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
344 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
345          130          135          140
347 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
349 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
350          145          150          155
352 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
354 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
355 160          165          170          175
357 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
359 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
360          180          185
362 cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtggg ggaacaaagg 636
365 ggagcctggt aaaaaacagc caagccccc agacctcagc ccaggcagaa gctgctctag 696
368 gacctggggc tctcagaggg ctcttctgcc atcccttgct tccctgaggc catcatcaaa 756
371 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816
374 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876
377 gctcttctc cctcactaa gaagacccaa acctctgcat aatgggattt gggcttttgt 936
380 acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaa aaaaaaa 993
384 <210> SEQ ID NO: 6
385 <211> LENGTH: 188
386 <212> TYPE: PRT
387 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
389 <400> SEQUENCE: 6
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394          20          25          30
396 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
397          35          40          45
399 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
400          50          55          60
402 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
403 65          70          75          80
405 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
406          85          90          95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/08/765,588A

DATE: 02/01/2001

TIME: 12:12:03

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date